

Patent 6,605,980

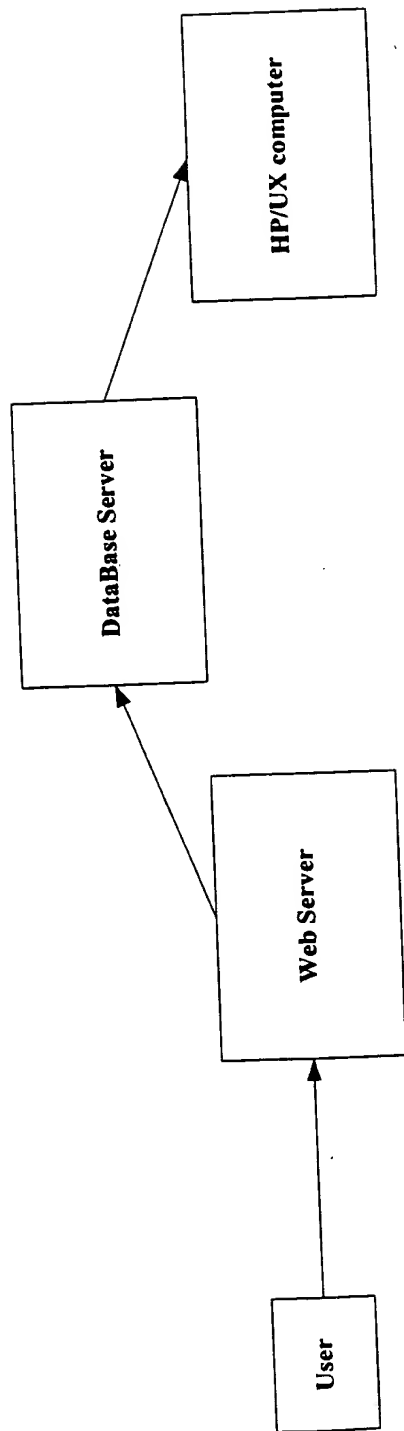


Fig 1

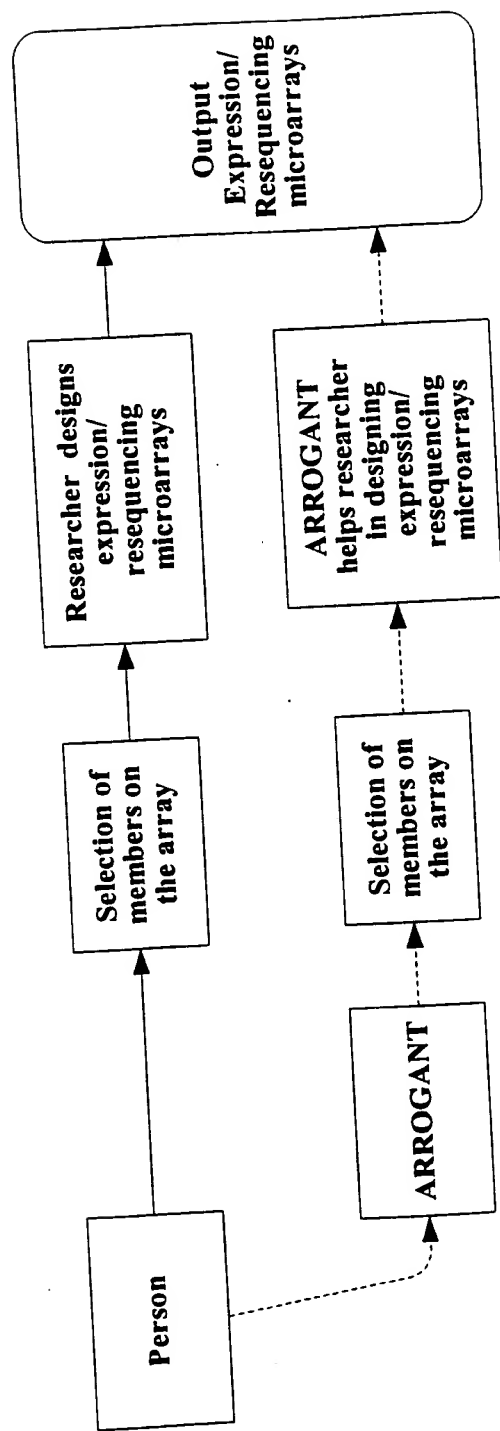


Fig 2

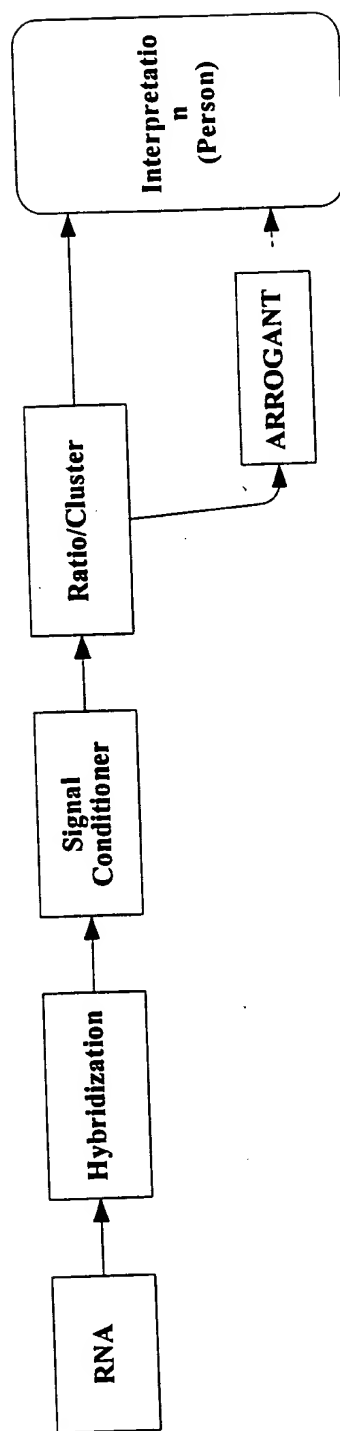


Fig 3

```

graph TD
    A[Final list of accession #'s] --> B[Unique list obtained]
    B --> C[Fasta files obtained using NCBI tools implemented locally]
    C --> D[BLASTable database created for the fasta files]
    C --> E[Each gene BLASTed against UniGene database]
    D --> F[Each gene BLASTed against this new BLASTable database]
    F --> G[Cross-Hybridization analysis obtained for sequences within the chip]
    E --> H[Total Cross-Hybridization analysis obtained]
    G --> I[Updated in the database]
    H --> I
  
```

Fig 4

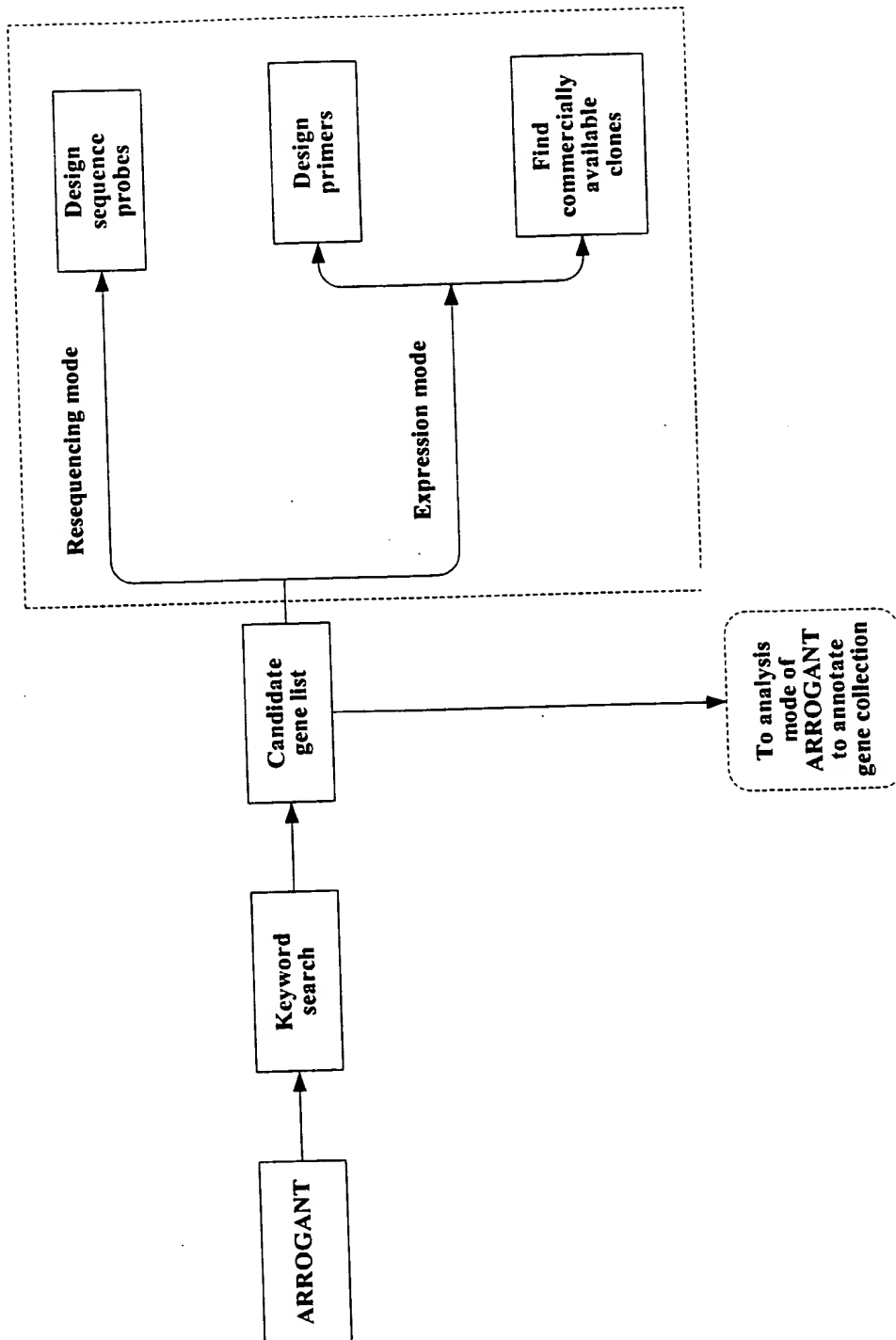


Fig 5

2) ARROGANT: Array Organizing Tool - Microsoft Internet Explorer

File Edit View Favorites Tools Help
Back Forward Stop Reload Home Search Favorites History Mail Print Edit Circuits
Links Address Book Autosync Bookmark Computers Extensions Indexing Top 20 Comparisons Health And Fitness
Address http://arrogant.swimed.edu/myweb/index.asp
For more information on any input see help or examples for help on options

click on Species

User Email: mailto:01@utsw.med.edu

Array Name: gga

Number of Array Members: 10 Use: ☐ Resequencing ☒ Expression

Source: ☐ PCR Products ☐ Gene Position: ☐ 3' Exon End Only
☐ Clones ☐ Random Exons
☒ Both

Keywords: candac hypetrathy

Databases:
☒ GenBank
☐ UniGene
☐ LocusLink
☐ KEGG
☐ KEGG Pathway
☐ Research Genetics

Status 26/12/00 5:50 PM 5MB 98% 11:11 AM

Fig 6

Accession Results - Macrosoft Internet Explorer

File Edit View Favorites Tools Help

Back Forward Stop Reload Home Search Favorites History Mail Mail Mail
[Links](#) [My Links](#) [Auto](#) [Blah blah](#) [CompuLink](#) [Entertainment](#) [Games](#) [Top](#) [Gaming](#) [Communications](#) [Health And Fitness](#)

Address [http://anagari.sarned.edu/mywebflysearcher.asp](#)

GO: 1 2 3 4 5 6 7 8 9 10

Record	Accession No	Definition	Organism
1	A32415	H.sapiens PAI-2 cDNA in pDBP1.	Homo sapiens
2	AA062310	m164f06.r1 Stratagene mouse kidney (#937315) Mus musculus cDNA clone IMAGE:516803 5' similar to WP:C40H1.6 CE00114 ;, mRNA sequence.	Mus musculus
3	AA073008	mm94c09.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:536080 5' similar to gb:M22810 Mouse androgen-regulated protein mRNA, complete cds (MOUSE);, mRNA sequence.	Mus musculus
4	AA073010	mm94c11.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:536084 5', mRNA sequence.	Mus musculus
5	AA073011	mm94c12.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:536086 5' similar to gb:X70847	Mus musculus

Print Print Preview Close

Status Bar 66 127 0.0 53 BCL Sel C Librar... [A] Annot... [B] Map... [C] Graphs [D] Maps [E] Index [F] Help [G] 11:18 AM

Fig 7

Form 06059300

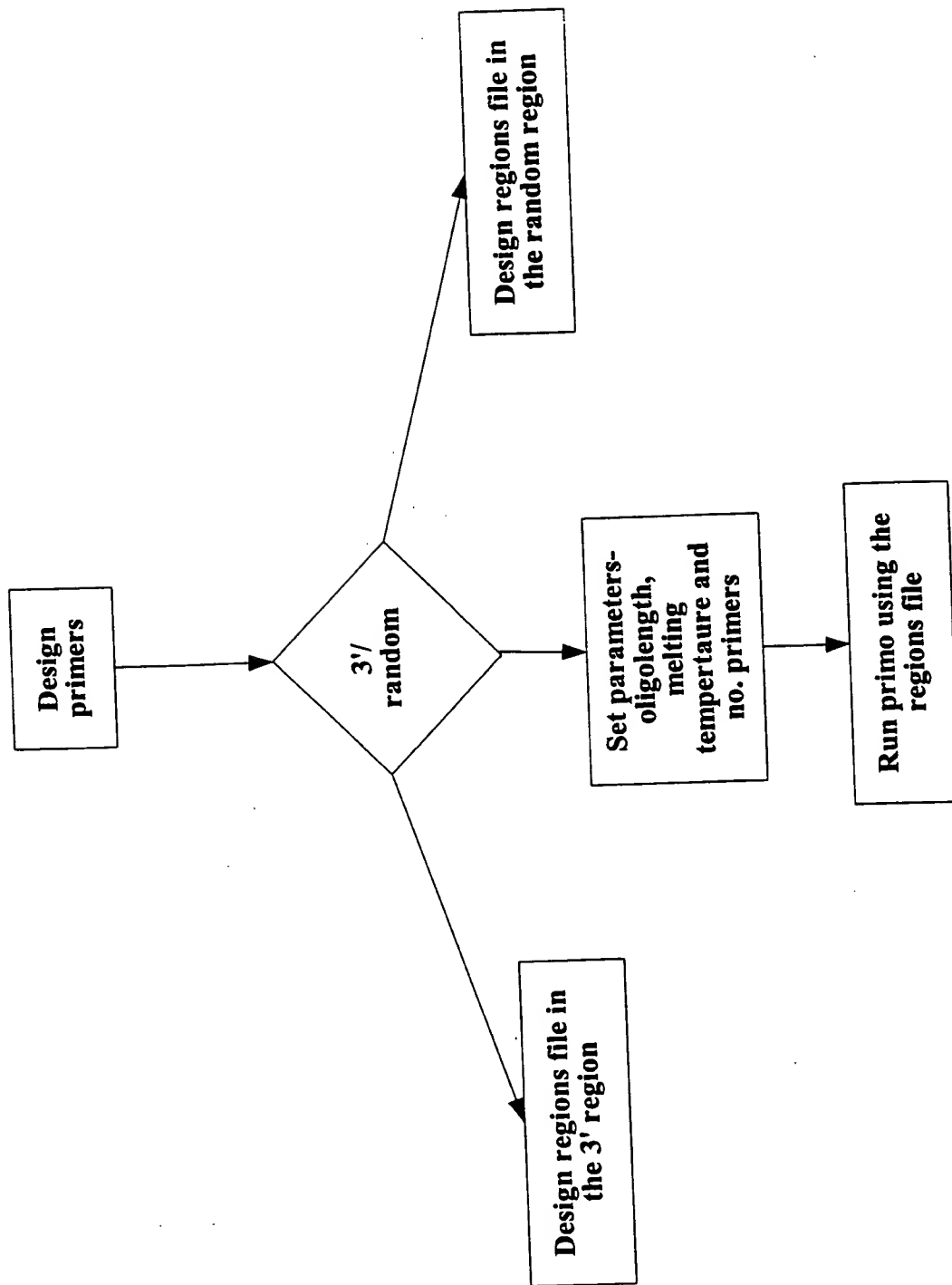


Fig 8

FOI b6 b7C b7D

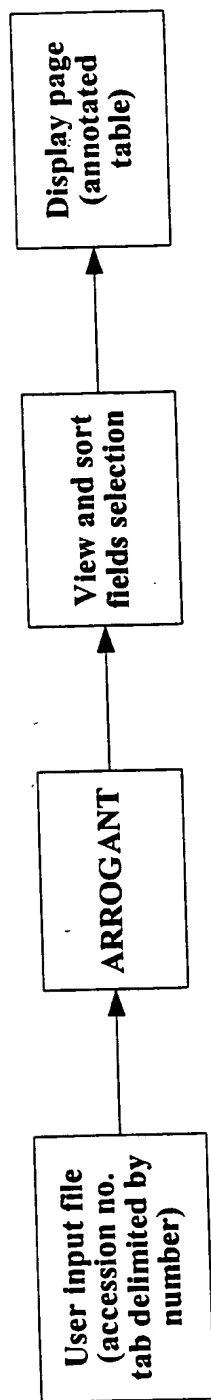


Fig 9

107250" 06059860

Select the fields you want to view, select how you would like to sort the data and press

Show Collection

<input type="checkbox"/> Accession	<input type="checkbox"/> IMAGE Identifier	<input type="checkbox"/> Alias protein
<input type="checkbox"/> Expression level data	<input type="checkbox"/> Xhyb analysis	<input type="checkbox"/> Phenotype
<input type="checkbox"/> Unique Identifier	<input type="checkbox"/> Issues	<input type="checkbox"/> Phenotype ID/ OMIM ID
<input type="checkbox"/> Title	<input type="checkbox"/> GDB	<input type="checkbox"/> Chromosome
<input type="checkbox"/> PubMed	<input type="checkbox"/> Gene name	<input type="checkbox"/> Map location
<input type="checkbox"/> Related Proteins	<input type="checkbox"/> Gene Function	<input type="checkbox"/> Map link
<input type="checkbox"/> Related Sequences	<input type="checkbox"/> Synonyms	<input type="checkbox"/> Map type
<input type="checkbox"/> Taxonomy	<input type="checkbox"/> Pathway	<input type="checkbox"/> STS- marker name
<input type="checkbox"/> Repeats	<input type="checkbox"/> SNP analysis	<input type="checkbox"/> STS- chromosome
<input type="checkbox"/> Hairpin/Palindrome	<input type="checkbox"/> Unigene ID	<input type="checkbox"/> STS- ID
<input type="checkbox"/> Homology	<input type="checkbox"/> Locus ID	<input type="checkbox"/> Reviewed RefSeq
<input type="checkbox"/> Research Genetics Clone	<input type="checkbox"/> Alias symbol	<input type="checkbox"/> cDNA Source

Sort Preferences

1. ☐ Unigene ID
2. ☐ Locus ID
3. ☐ Reviewed RefSeq
4. ☐ Repeats
5. ☐ Chromosome

Fig 10

04:50" 06059860

Arrogant Server

Welcome to the ARROGANT (ARRAY ORGANIZING Tool) Server, please move back and forth between this page and the earlier page to chose the fields to be viewed and fields to be sorted on.

For more information on any input data field click on that link. For example, for help on Accession click on [Accession](#)

Databases Updated when?

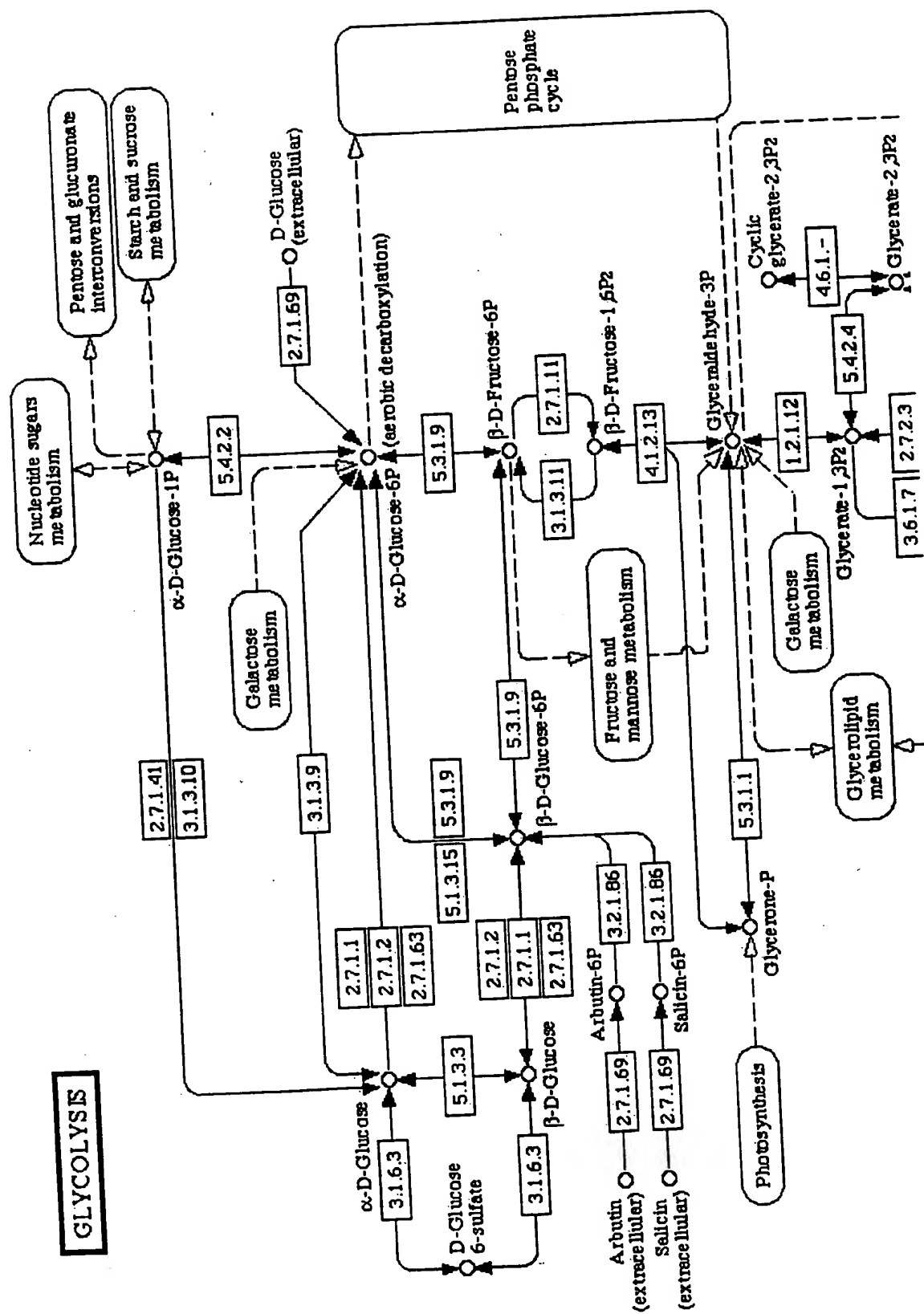
Database	Genbank	Pomposus	LocustHk	Unigene	Research Genetics
Last Updated	2/7/01 8:06:55 AM	1/18/01 8:35:24 AM	2/6/01 8:34:29 AM	1/28/01 8:34:45 AM	1/8/01 8:35:59 AM

Fig 11

Download results table in excel format

Results Table

Record	Accession	Uni ID	Cluster ID	Title	Homologs	Gene Type/Function
1	NM_000236	4557722	Hs.2994	Homo sapiens lipase, hepatic (LIPC), mRNA.	Mm.362 Rn.1195	Summary: LIPC encodes hepatic triglyceride lipase which is expressed in liver. LIPC has dual functions of triglyceride hydrolase and ligand, bridging factor for receptor mediated lipoprotein uptake
2	NM_000023	4506910	Hs.99231	Homo sapiens sarcoglycan, alpha (50kD dystrophin-associated glycoprotein) (SGCA), mRNA.	Mm.18709 Rn.23558	
Summary	239	232	207	232	201	239
Record	Accession	Uni ID	Cluster ID	Title	Homologs	Gene Type/Function



[illegible]

Column Name	Datatype	Length	Precision	Scale	Allow Null	Default Value
accsno	varchar	9	0	0		((-1))
nid	varchar	10	0	0	✓	((-1))
defn	varchar	255	0	0	✓	((-1))
type	varchar	100	0	0	✓	((-1))
dna	varchar	6	0	0	✓	((-1))
organism	varchar	25	0	0	✓	((-1))
source	varchar	25	0	0	✓	((-1))
keyword	varchar	6	0	0	✓	((-1))
comments	varchar	255	0	0	✓	((-1))
featstuff	varchar	1400	0	0	✓	((-1))
fstart	varchar	10	0	0	✓	((-1))
fend	varchar	10	0	0	✓	((-1))
species	varchar	200	0	0	✓	((-1))
authors	varchar	255	0	0	✓	((-1))
journal	varchar	255	0	0	✓	((-1))
version	varchar	30	0	0	✓	((-1))
reference	varchar	25	0	0	✓	((-1))
title	varchar	100	0	0	✓	((-1))
basepair	varchar	10	0	0	✓	((-1))

Fig 13

104250" 06059860

Metadata	
clusterid	
accession	
type	

UniProt	
clusterid	
pro org	
pro id	
similarity	

UniProt	
clusterid	
otherproids	

UniProt	
UG	
express	
locuslink	
title	
gene	
cytoband	
sts	
mqi	
chromosome	

UniProt	
UG	
tissue	

Fig 14

T04250" 06059860

kegg	
	Uniqueld
	Locusid
	Organism
	Name
	Defn
	class
	position
	gdb
	ncbi

lookpath	
	pathno
	pathway

Fig 16

homoortho	
	Unigld1
	Unigld2
	Loid1
	Loid2
	Acc1
	Acc2

Fig 17

098590.05401

RG_Hs_seq_ver_101100	
<input checked="" type="checkbox"/>	[Release Number]
<input type="checkbox"/>	[RG Plate]
<input type="checkbox"/>	[RG row]
<input type="checkbox"/>	[RG column]
<input type="checkbox"/>	[Insert Size*]
<input type="checkbox"/>	[Cluster ID]
<input type="checkbox"/>	[UG build]
<input type="checkbox"/>	[Clone ID]
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<input type="checkbox"/>	Tissue
<input type="checkbox"/>	Library
<input type="checkbox"/>	Accession
<input type="checkbox"/>	NID
<input type="checkbox"/>	[Gene Name]
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<input type="checkbox"/>	Chromosome
<input type="checkbox"/>	Band
<input type="checkbox"/>	Markers
<input type="checkbox"/>	Col019
<input type="checkbox"/>	Barcode
<input type="checkbox"/>	Antibiotics
<input type="checkbox"/>	[repeat ?]

Fig 18

• •

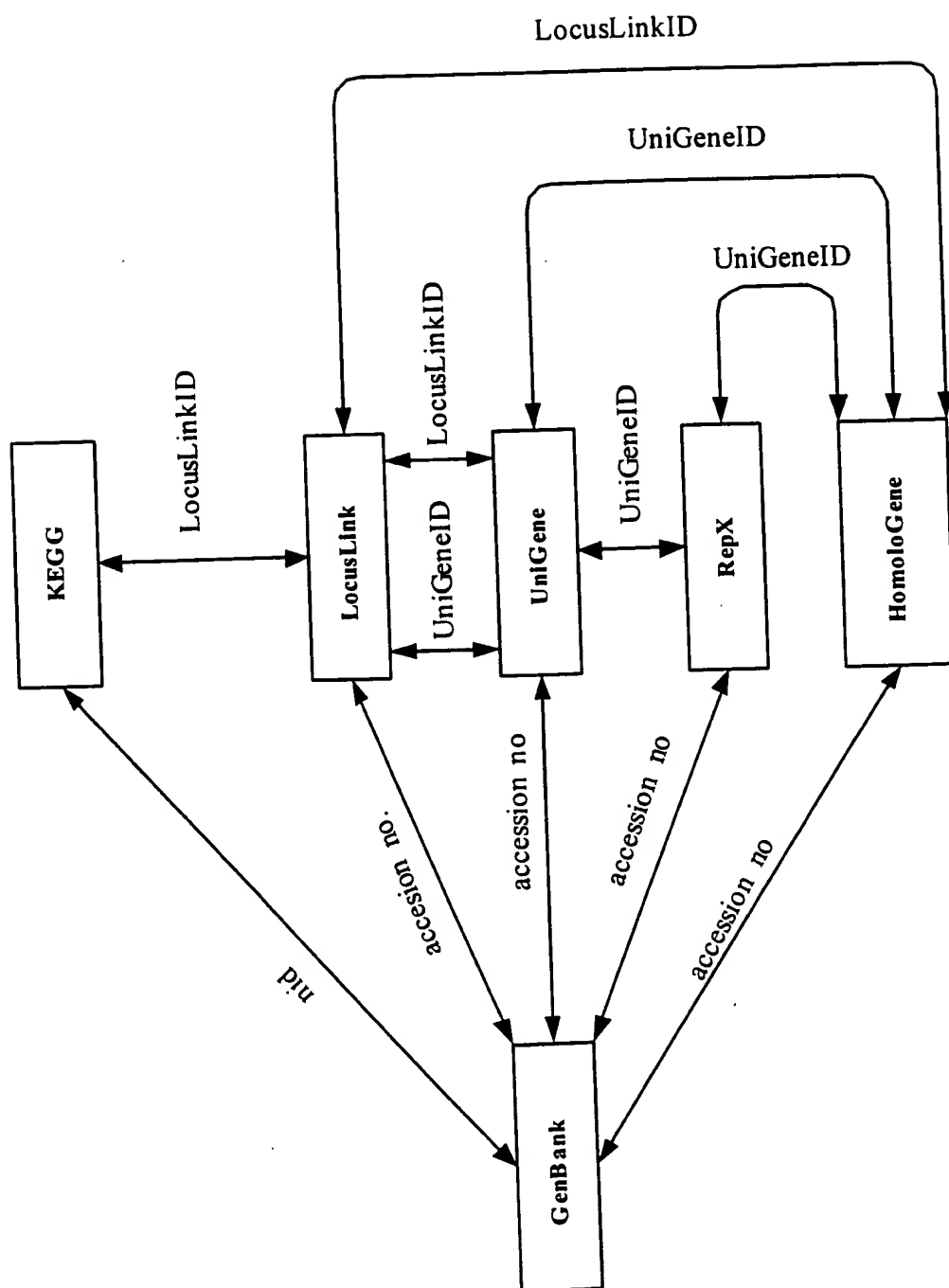


Fig 19

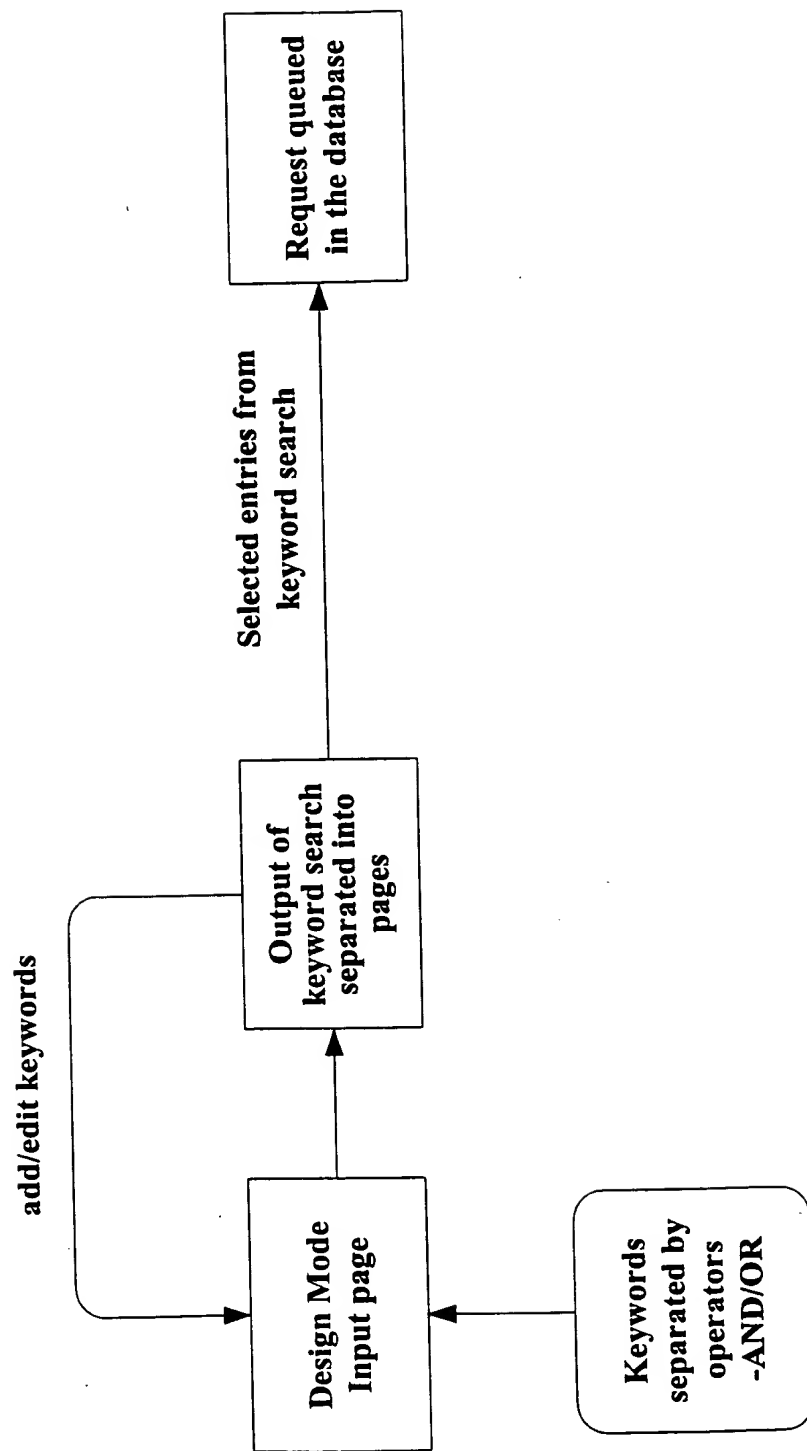
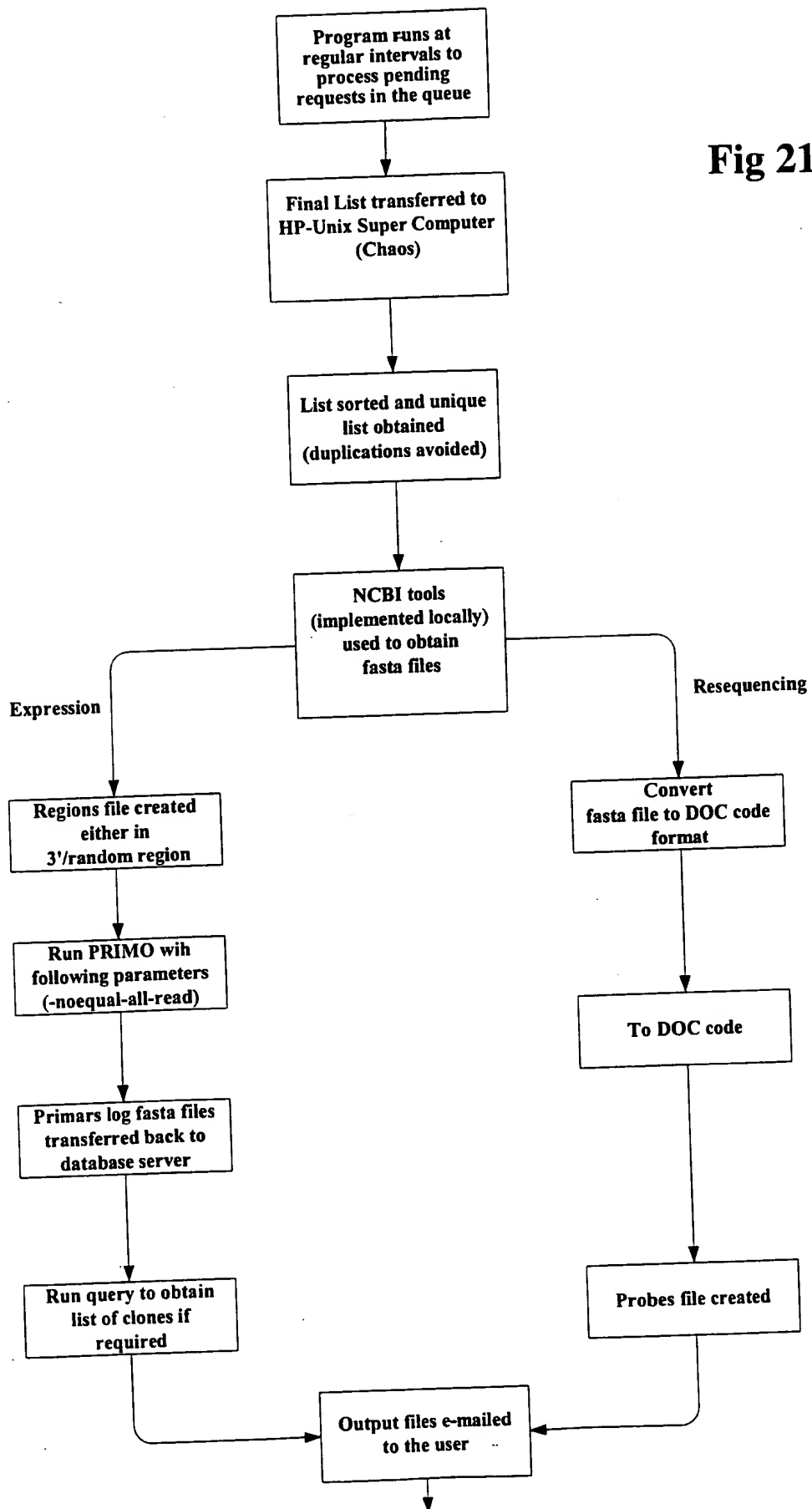


Fig 20

SECRET



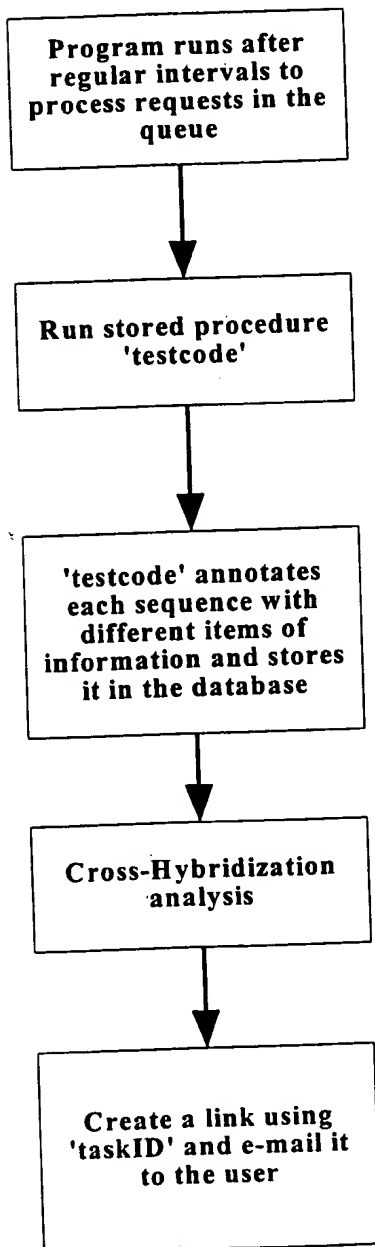
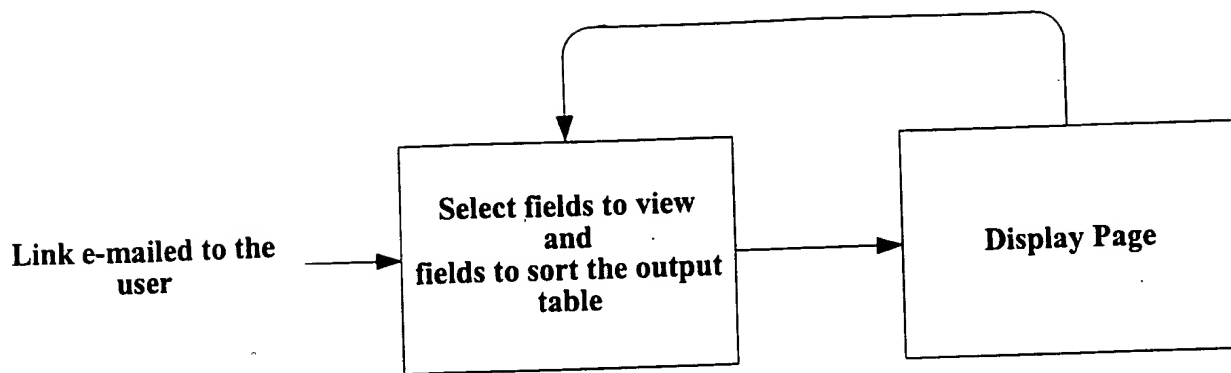


Fig 22

09865090.052401

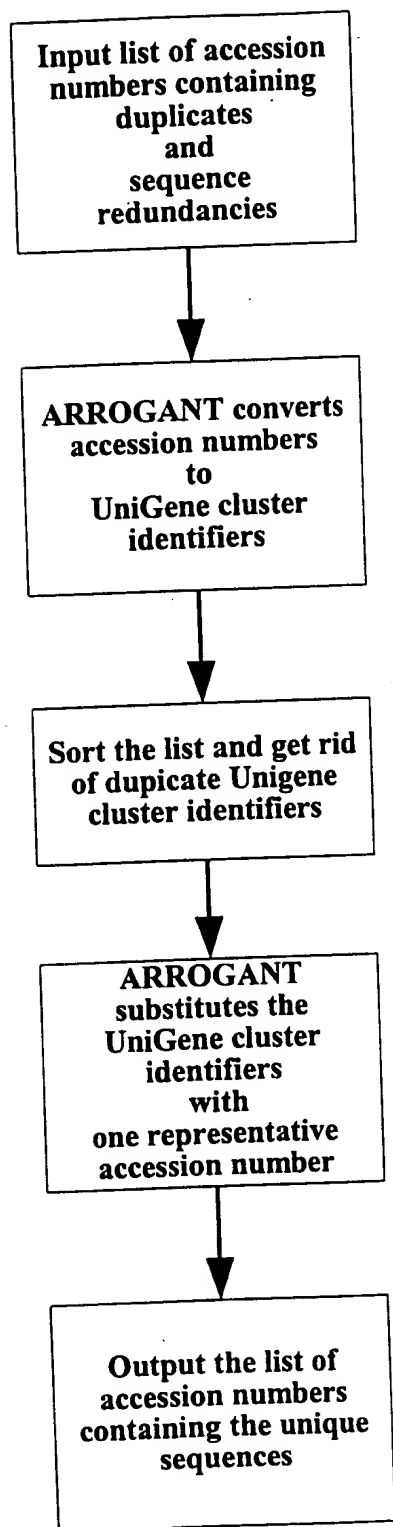


Fig 23

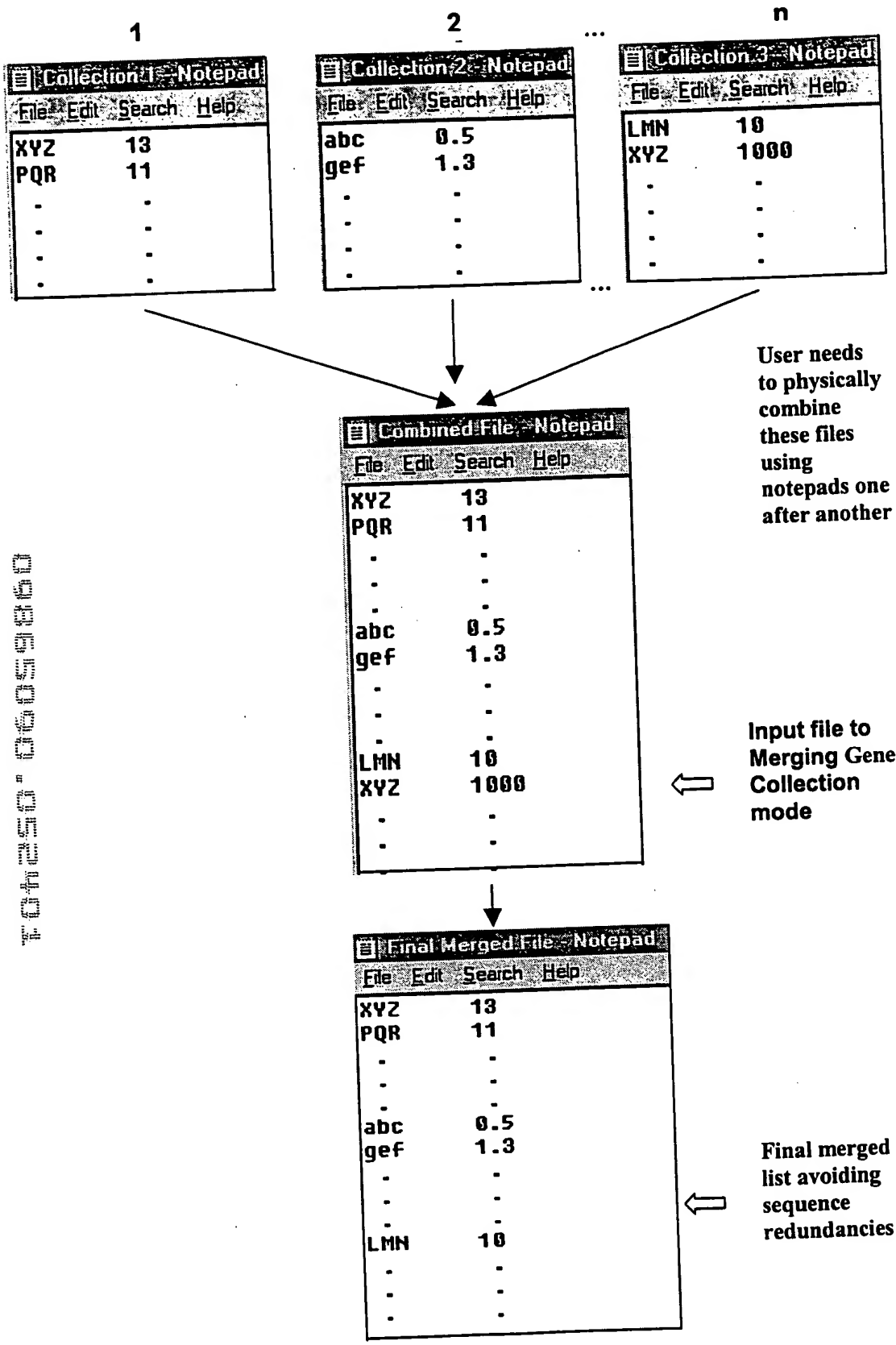


Fig 24

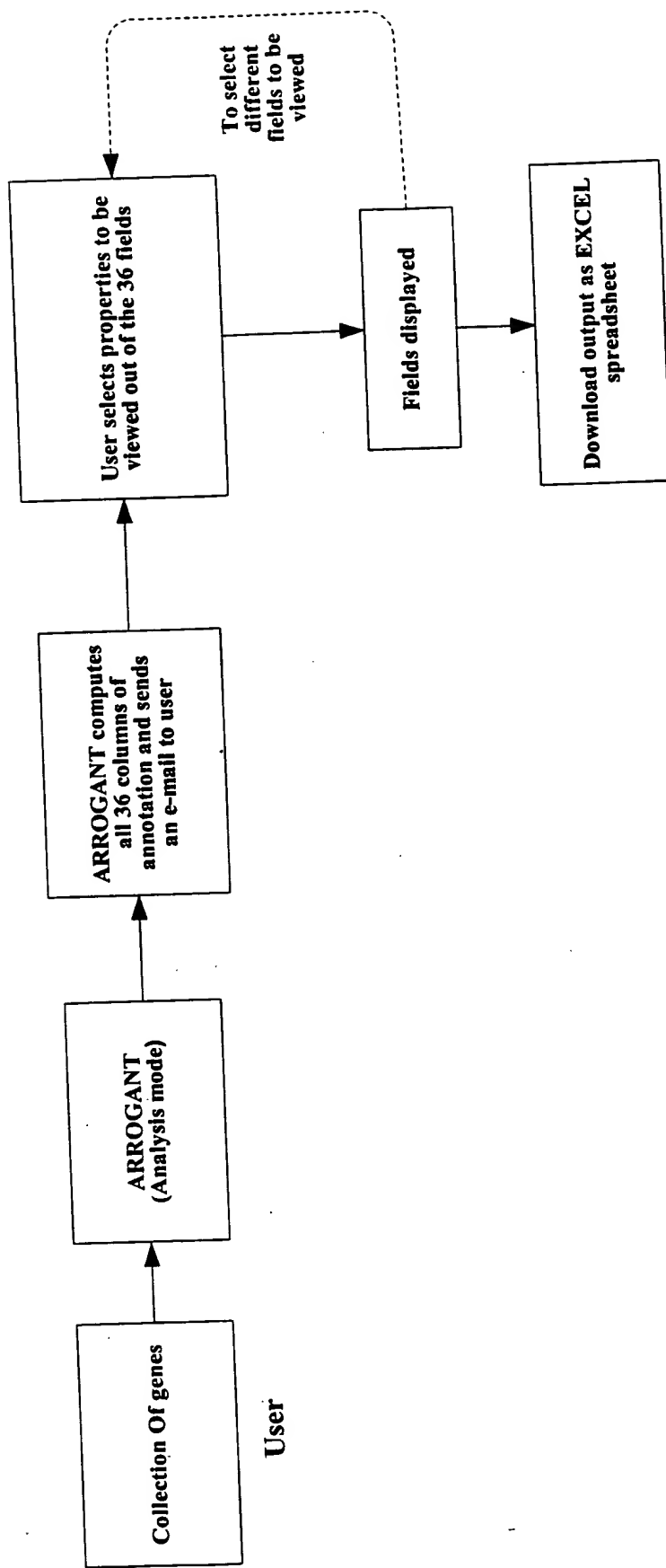


Fig 25

Form 00059860

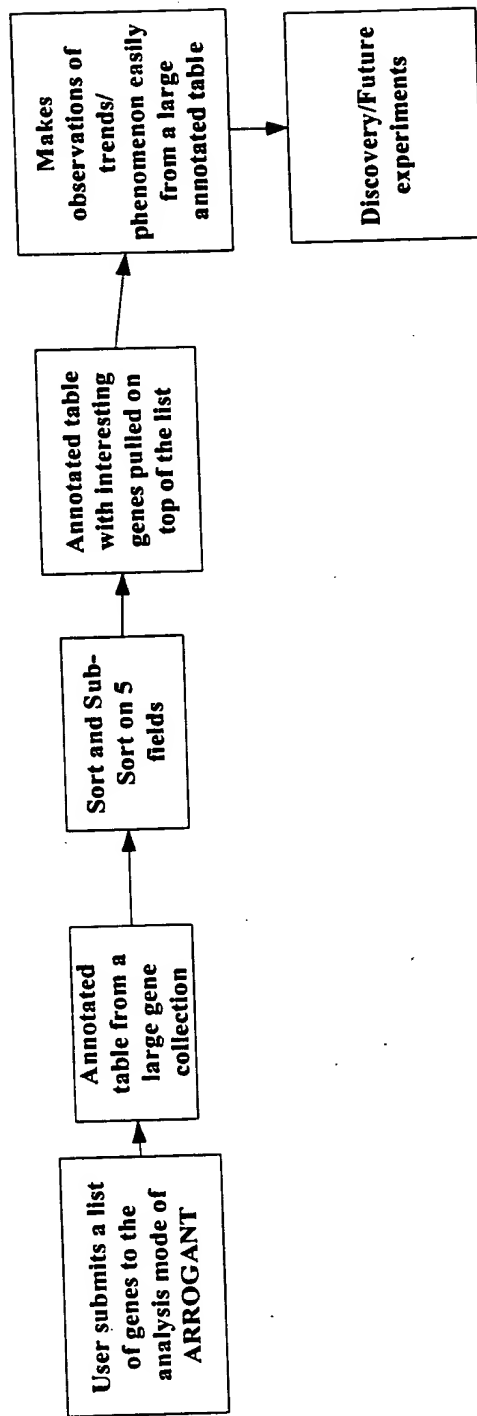


Fig 26

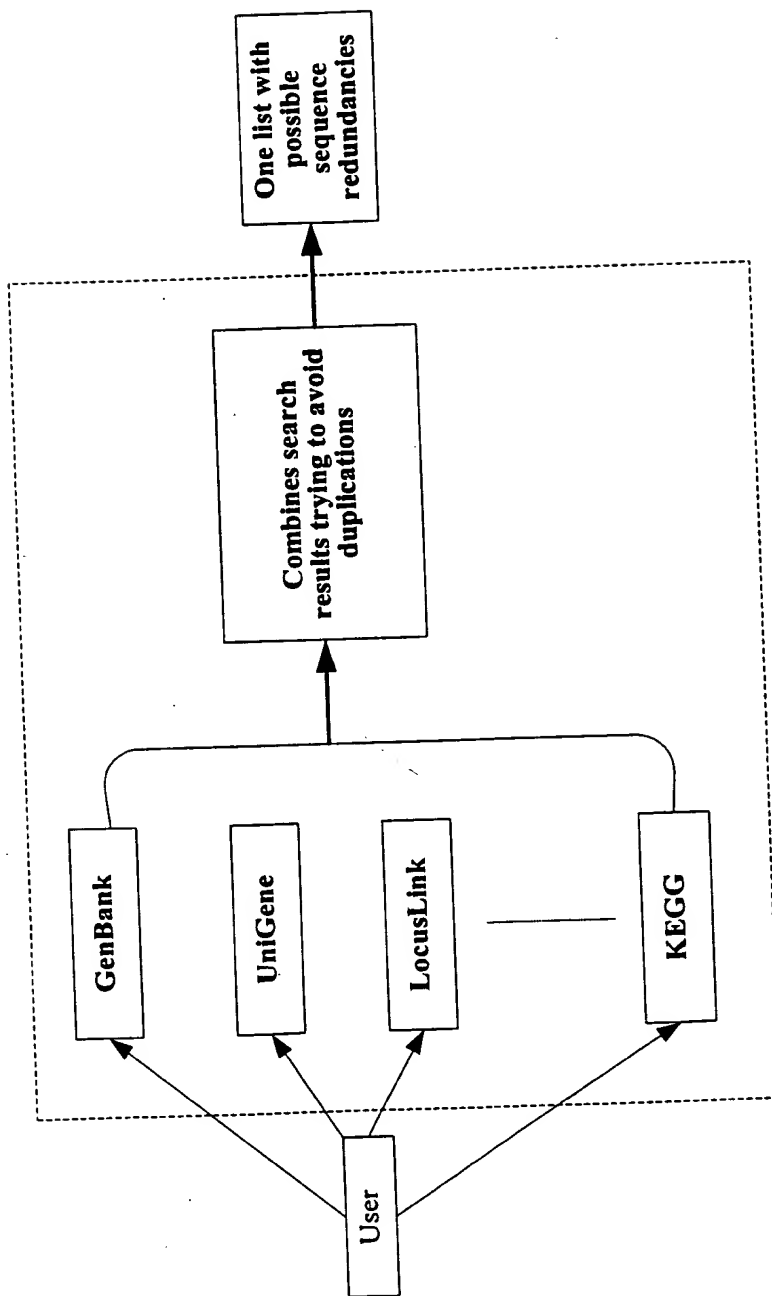
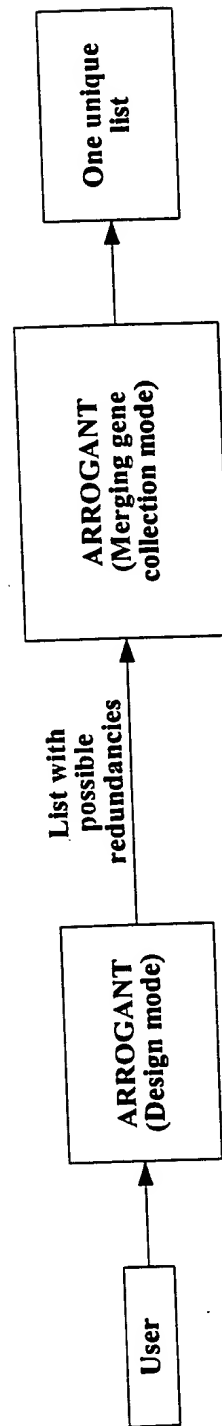


Fig 27



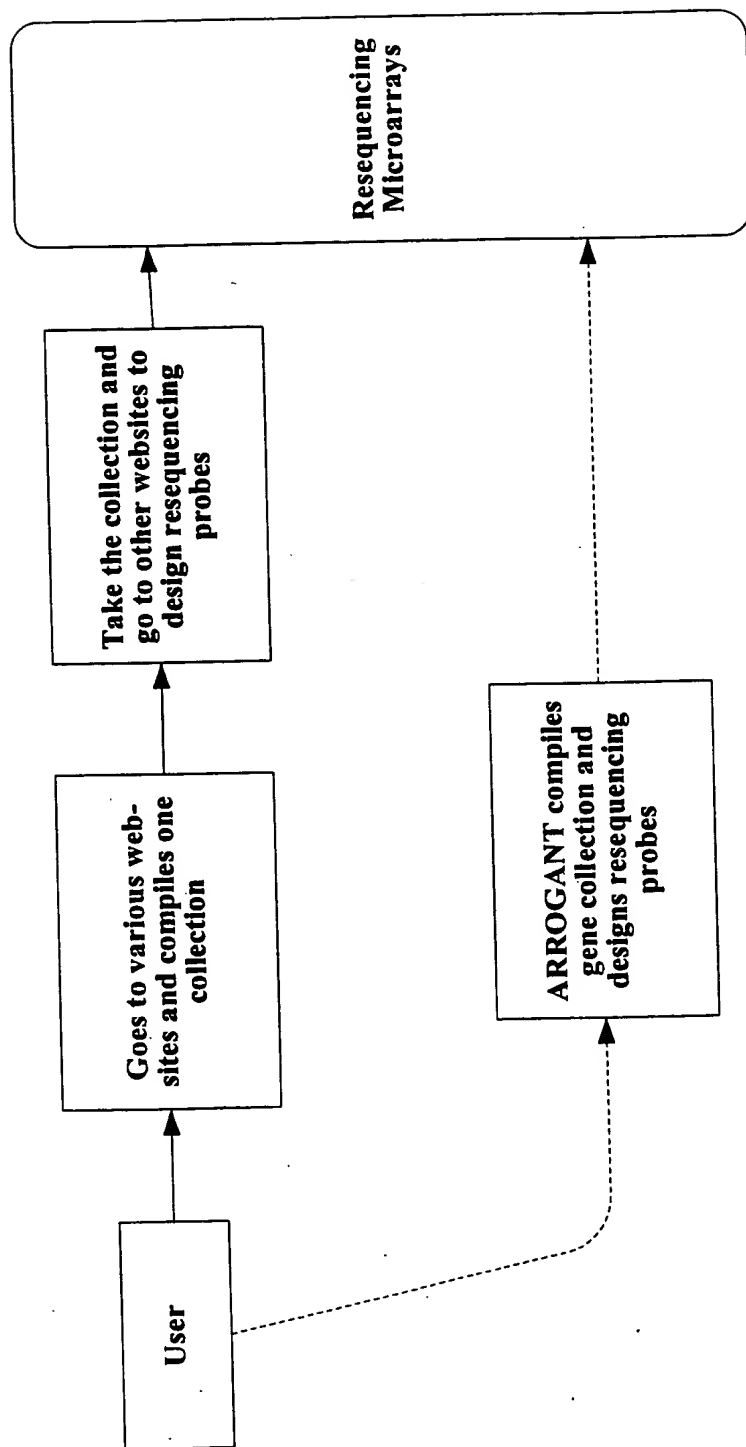


Fig 28

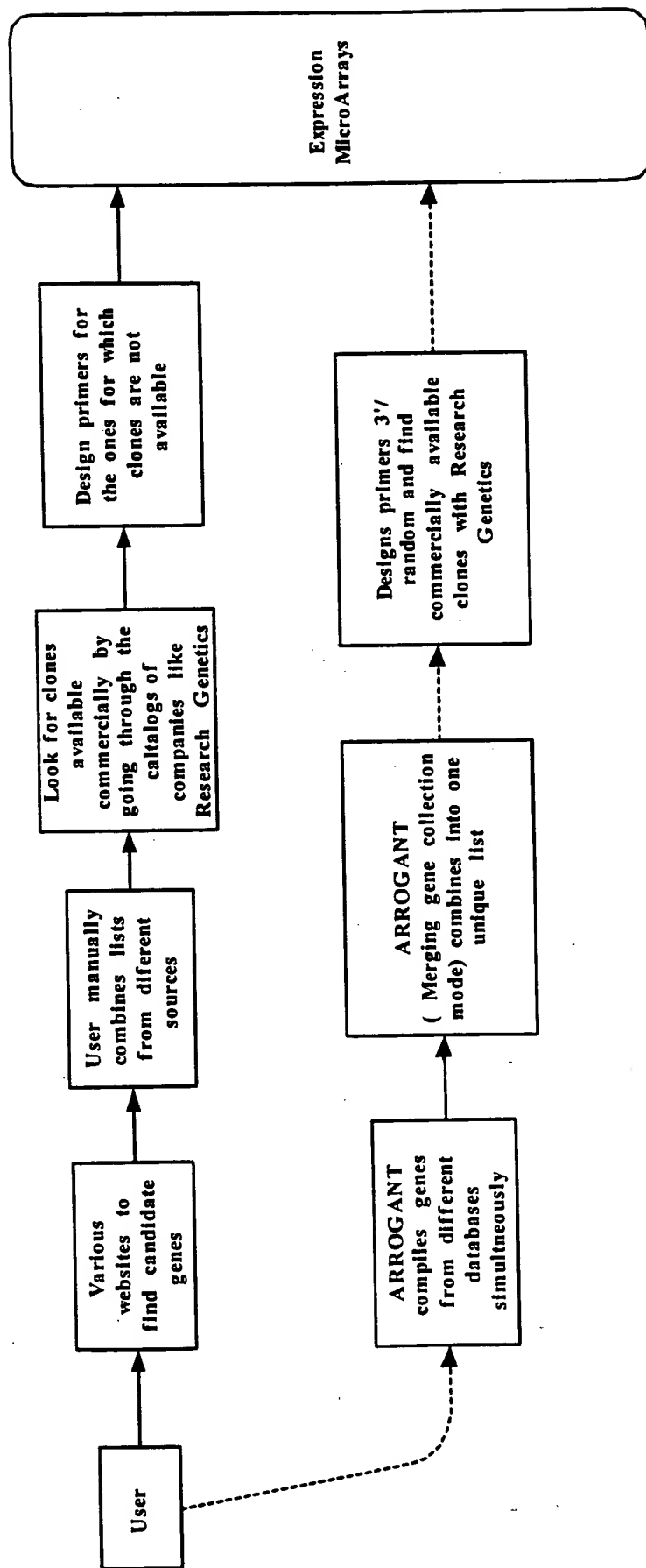


Fig 29

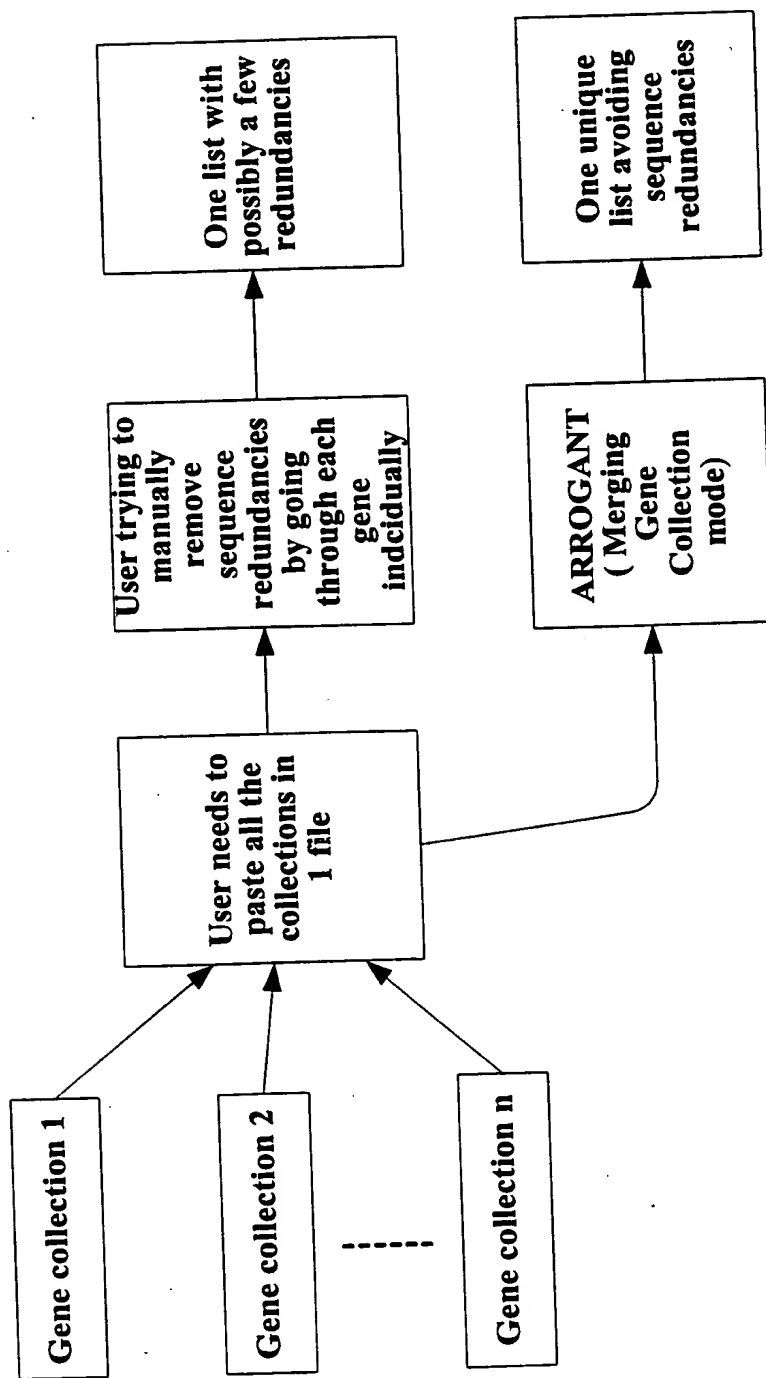


Fig 30

```
graph LR; A[Microarray results] --> B[Researcher interprets the results]; A -.-> C["ARROGANT (analysis mode) tags the potential false positives caused due to cross-hybridization"]; C -.-> B
```

```
graph LR; A[Members to be included on the expression micro-array] --> B[Design primers to amplify sequences to be spotted on the]; A -.-> C[ARROGANT tags the regions causing potential cross-hybridization]; C -.-> B;
```

The flowchart illustrates the ARROGANT process for microarray design. It begins with a box labeled "Members to be included on the expression micro-array". A solid arrow points from this box to a box labeled "Design primers to amplify sequences to be spotted on the". A dashed arrow points from the first box down to a box labeled "ARROGANT tags the regions causing potential cross-hybridization". A dashed arrow then points from this box up to the "Design primers" box, indicating a feedback loop.

Fig 31b